



ARACHNOBASE WHITE PAPER 2025

ARACHNOBASE: AN ARACHNID GENOMICS KNOWLEDGEBASE FOR THE FUTURE

Arachnobase Community Members (*Listed in Section 4.1*),

Saoirse Foley. Marian University, USA. schioedtei@gmail.com

PURPOSE

This document serves to outline the authors' intention to launch Arachnobase: a model organism knowledgebase for arachnids. Arachnobase aims to integrate high-quality genomic and computational data for taxa across different arachnid orders in adherence with FAIR principles (Findable, Accessible, Interoperable, and Reproducible) to support ongoing research efforts, particularly in the fields of evolution and development. Arachnobase will therefore serve both the large, global arachnid research community, and also be of benefit to other biologists, particularly those with interests in comparative genomics. This white paper identifies the current needs of the arachnological research community, with proposals on how Arachnobase can support such efforts.

TABLE OF CONTENTS

1. Impact of the Arachnid Research Community	1
1.1. Arachnids as emergent model organisms for experimental biology	1
1.2. Biotechnology applications derived from arachnids	2
1.3. Current status of arachnid genomes	3
2. Arachnobase: Progress to Date	4
2.1. Broad vision for Arachnobase	4
2.2. Community survey has identified research needs	4
2.3. Community survey has identified initial species for support	6
2.4. Some computational infrastructure has been secured	7
3. Arachnobase: Specific Aims	7
3.1. Gene pages	7
3.2. Gene orthology mapping and gene identities	7
3.3. Genome browser tracks for visualization	8
3.4. FAIR principles and integrating with other resources	8
3.5. Arachnid community hub	9
3.6. Additional Arachnobase functions	9
3.7. Future directions	9
4. Additional Information	11
4.1. Arachnobase community members	11
4.2. References	12

1. IMPACT OF THE ARACHNID RESEARCH COMMUNITY

1.1. Arachnids as emergent model organisms for experimental biology

Arachnids are emerging as model systems to study an array of biological processes, such as developmental patterning, behavior, neurobiology, and the origin of complex traits (e.g. McGregor et al., 2008; Oda and Akiyama-Oda 2008; Hilbrant et al., 2012; Schwager et al., 2015; Oda and Akiyama-Oda, 2020). As an ancient, diverse, and early-branching arthropod clade, they make excellent candidates for interrogating macroevolutionary processes as well as biological processes at the population level. Many arachnid systems possess desirable qualities that make them a good choice for conducting developmental, neurobiological, behavioral, and evolutionary research, including:

- High fecundity (*hundreds, sometimes thousands of offspring*)
- Quick to mature in many tractable species (*Opiliones may reach maturity in less than two months post-hatching*)
- Hardiness and tractability in captivity
- Modest, inexpensive housing and maintenance of live specimens
- Largely display their natural behavior in captivity
- Availability of genomics resources (*transcriptomes; chromosome-level genomes*)
- Availability of functional tools (crosses; RNA interference; CRISPR; single-cell RNA-Seq)
- Abundance and accessibility for researchers (*particularly synanthropic species like *P. tepidariorum**)

A select number of key studies that highlight recent breakthroughs in arachnids are listed here by category:

Embryogenesis and Developmental Patterning

Gainett, *Frontiers in Zoology* 2022. <https://pubmed.ncbi.nlm.nih.gov/35246168/>
Iwasaki-Yokozawa, *BMC Biology* 2022. <https://pubmed.ncbi.nlm.nih.gov/36203191/>
Klementz, *bioRxiv* 2025. <https://doi.org/10.1101/2025.07.08.663771>
Pechmann, *eLife* 2017. <https://pubmed.ncbi.nlm.nih.gov/28849761/>
Propistsova, *EvoDevo* 2025. <https://pubmed.ncbi.nlm.nih.gov/40057742/>
Setton, *Journal of Arachnology* 2019. <https://doi.org/10.1636/JoA-S-18-081>

Cell Signaling Pathways

Akiyama-Oda, *Science Advances* 2020. <https://pubmed.ncbi.nlm.nih.gov/32917677/>
Medina-Jiménez, *EvoDevo* 2024. <https://pubmed.ncbi.nlm.nih.gov/39327634/>
Wang, *Science Advances* 2023. <https://pubmed.ncbi.nlm.nih.gov/38117895/>

Homeobox Gene Neofunctionalization

Aase-Remedios, *Molecular Biology and Evolution* 2023. pubmed.ncbi.nlm.nih.gov/37935059/
Janeschik, *Frontiers in Ecology and Evolution* 2022. <https://doi.org/10.3389/fevo.2022.810077>
Leite, *Molecular Biology and Evolution* 2018. <https://pubmed.ncbi.nlm.nih.gov/29924328/>

Rare Genomic Changes

Gainett, *Evolution & Development* 2023. <https://pubmed.ncbi.nlm.nih.gov/38124251/>
Nolan, 2020. <https://pubmed.ncbi.nlm.nih.gov/31927629/>
Ontano, *Molecular Biology and Evolution* 2021. <https://pubmed.ncbi.nlm.nih.gov/33565584/>

Genetics and Comparative Genomics

Harper, *G3* 2021. <https://pubmed.ncbi.nlm.nih.gov/34849767/>
Hendrickx, *Nature Ecology and Evolution* 2022. <https://pubmed.ncbi.nlm.nih.gov/34949821/>
Kulkarni, *Journal of Heredity* 2025. <https://pubmed.ncbi.nlm.nih.gov/39679458/>
Schwager, *BMC Biology* 2017. <https://pubmed.ncbi.nlm.nih.gov/28756775/>
Thomas, *Genome Biology* 2020. <https://pubmed.ncbi.nlm.nih.gov/31969194/>

Neuroscience and Behavior

Corver, *Current Biology* 2021. <https://pmc.ncbi.nlm.nih.gov/articles/PMC8612999/>
Rößler, *PNAS* 2022. <https://pubmed.ncbi.nlm.nih.gov/35939710/>
Jin, *Nature Ecology and Evolution* 2023. <https://pubmed.ncbi.nlm.nih.gov/37919396/>

The genomic resources generated from efforts such as these have also contributed substantially towards phylogenomic and Tree of Life research efforts.

1.2. Biotechnology applications derived from arachnids

Arachnids are particularly noteworthy for the plethora of biomaterials that continue to inspire new biotechnologies with applications in human health and wellbeing. A select number of key studies are listed here by category:

Parasite Genomics and Adaptations

Jia, *Cell* 2020. <https://pubmed.ncbi.nlm.nih.gov/32814014/>
Rolandelli, *Nature Communications* 2024. <https://pubmed.ncbi.nlm.nih.gov/38459063/>
Xiong, *Molecular Biology and Evolution* 2022. <https://pubmed.ncbi.nlm.nih.gov/35535514/>

Silk Evolution and Applications

Arakawa, *Science Advances* 2022. <https://pubmed.ncbi.nlm.nih.gov/36223455/>
Ayoub, *Integrative & Comparative Biology* 2021. <https://pubmed.ncbi.nlm.nih.gov/34003260/>
Frandsen, *PNAS* 2023. <https://pubmed.ncbi.nlm.nih.gov/37094147/>
Wu, *Nature Communications* 2024. <https://pubmed.ncbi.nlm.nih.gov/38789409/>

Venom Evolution and Profiling

Dresler, *Frontiers in Arachnid Science* 2024. <https://doi.org/10.3389/frchs.2024.1445500>
Erkoc, *iScience* 2024. <https://pubmed.ncbi.nlm.nih.gov/39021791/>
Lyons, *Biology Letters* 2025. <https://pubmed.ncbi.nlm.nih.gov/40393515/>

Website and Database Resources for Arachnid Research

Baradaran, *Toxins* 2024. <https://pubmed.ncbi.nlm.nih.gov/39591252/>
Castoe, *Integrative Organismal Biology* 2025. <https://pubmed.ncbi.nlm.nih.gov/40661153/>
Pekár, *Database* 2021. <https://pubmed.ncbi.nlm.nih.gov/34651181/>

1.3. Current status of arachnid genomes

A summary of currently available arachnid genomes as of 18th July 2025 is given in Table 1. When querying the search term “Arachnida” on the NCBI Genome datasets tool (available here: <https://www.ncbi.nlm.nih.gov/datasets/genome>), 331 results are returned. However, when the search parameters are refined to only contain entries from 2024-25, we see 108 entries—almost a third of the total. Most of these genome entries are dominated by three main groups: mites (Acariformes), ticks (Parasitiformes), and spiders of the infraorder Araneomorphae. These are the only three orders that contain genomes with both a chromosome-level assembly and a RefSeq annotation.

ORDER	LEVEL	REFSEQ	NUMBER	SINCE 2024
Araneae (Araneomorphae)	Chromosome	Yes	78	33 (~42%)
Araneae (Mygalomorphae)	Chromosome	No	6	5 (~83%)
Araneae (Liphistiidae)	Scaffold	No	1	1 (100%)
Scorpiones	Scaffold	Yes	4	0 (0%)
Pseudoscorpiones	Chromosome	No	2	0 (0%)
Schizomida	Scaffold	No	1	1 (100%)
Amblypygi	NA	NA	0	NA
Uropygi	Chromosome	No	1	1 (100%)
Palpigradi	NA	NA	0	NA
Opiliones	Chromosome	No	6	3 (50%)
Ricinulei	NA	NA	0	NA
Solifugae	Chromosome	No	1	1 (100%)
Acariformes	Chromosome	Yes	128	16 (~12%)
Parasitiformes	Chromosome	Yes	103	47 (~46%)
TOTAL			331	108 (~33%)

Table 1: Arachnid Genomes Available Via NCBI Genome Datasets Tool (as of 18th July 2025). “Order” refers to the arachnid order in question, with spiders being partitioned into their three infraorders. Orders comprising the Arachnoplumonata clade have their names shaded in grey. “Level” refers to the best available resolution of a genome within that order. “RefSeq” refers to whether any genome for that order has been through the NCBI Eukaryotic Genome

Annotation Pipeline. “Number” refers to the total number of genomes available on the resource. “Since 2024” denotes how many of the genomes available were submitted from the year 2024 onwards, followed by a percentage expressing that proportion.

This paints a rather polarized and biased picture of the arachnid genome landscape. On one hand, there has been a huge influx of arachnid genomes over the past year alone. Many arachnid orders have had their first genomes published since the beginning of 2024, which is most encouraging. With sequencing technologies becoming more accessible, we must expect that this is likely to continue. On the other hand, there are entire arachnid orders that remain without a published genome.

Ideally, a genome would be highly resolved (i.e. chromosome-level) and annotated in such a way that it is interoperable across different resources. The NCBI Eukaryotic Genome Annotation Pipeline facilitates RefSeq annotation, which systematically organizes molecular data to uniquely identify genomic molecules across NCBI and other resources (details here: https://www.ncbi.nlm.nih.gov/refseq/annotation_euk/process/). To this end, Table 1 provides an overview of some deficiencies with the currently available selection of arachnid genomes. Many orders (e.g. Solifugae) have chromosome-level assemblies, but lack an interoperable annotation. Others (e.g. Scorpiones) have interoperable RefSeq annotations, but are not sequenced to a resolution beyond scaffolds.

2. ARACHNOBASE: PROGRESS TO DATE

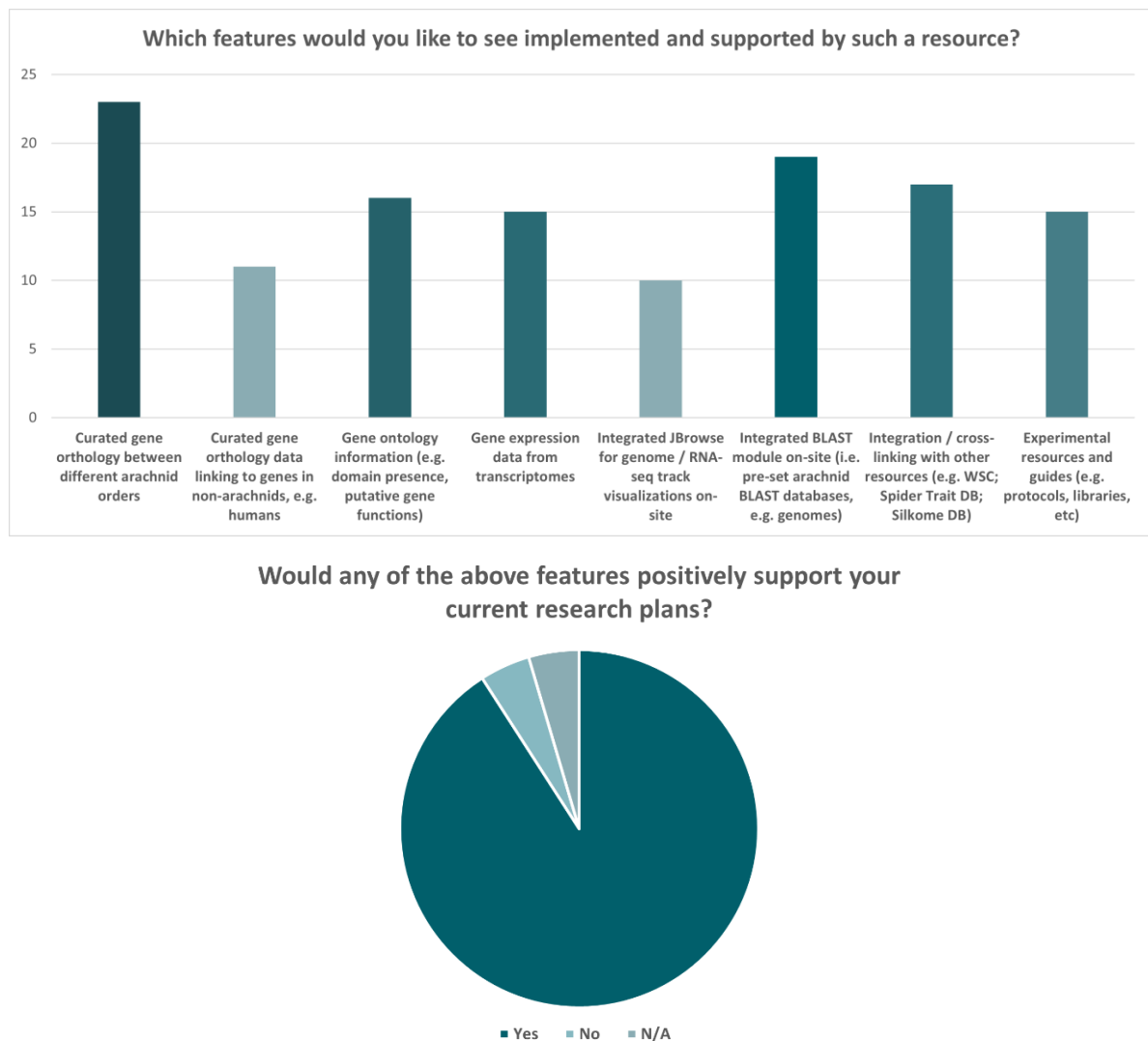
2.1. Broad vision for Arachnabase

It is intended for Arachnabase to one-day function like a mature model organism database, e.g. Xenbase (Fisher et al., 2023) and FlyBase (Öztürk-Çolak et al., 2024), and to support research endeavors worldwide in the same way that the aforementioned resources and others continue to do. Recently, Echinobase (Arshinoff et al., 2021) demonstrated success in leveraging existing knowledgebase infrastructure to quickly and efficiently deploy a feature-rich resource for the echinoderm research community. It is intended for this same, proven process to be leveraged for Arachnabase.

2.2. Community survey has identified research needs

In June 2024, a survey was disseminated by email via the International Society of Arachnology to assess interest in Arachnabase and collect information on which features would provide the greatest value to researchers. Some of these needs were anticipated given ongoing discourse in the arachnid research community (Garb et al., 2018; Kuntner 2022). Results from 24 survey responses are summarized in Figure 1.

Figure 1: Community survey results



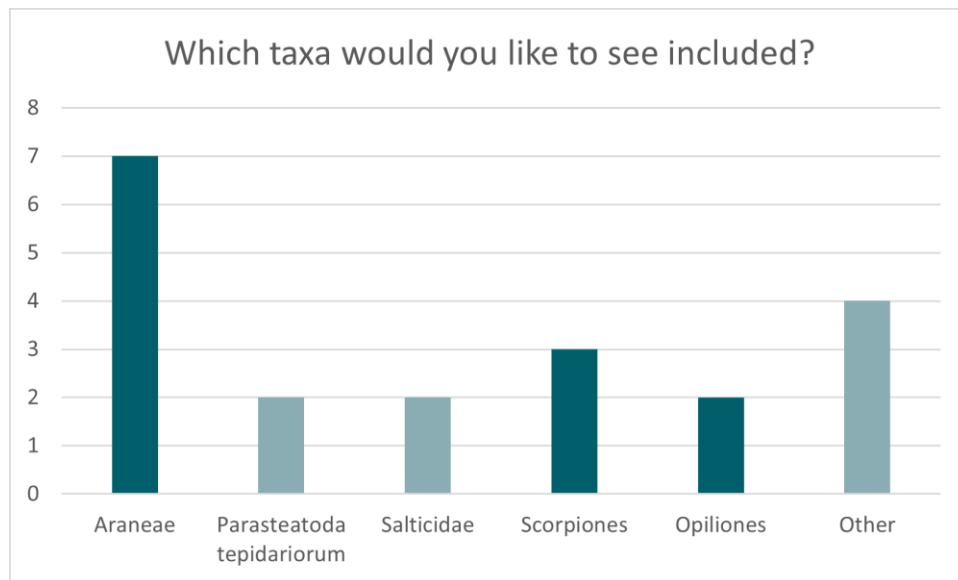
When responding to the question on whether any of the above features would positively support current research plans, respondents were also given a free space to type and specify what they are working on and how these features could help. Many respondents noted the value in having curated data that cross-links with other resources, and one respondent noted that having all of the above in one centralized place would be useful. Some active areas of community research that Arachnobase could support were identified from this part of the survey, and are summarized below:

- Diversity of scorpion venoms
- Evolution of spider venom genes
- Arachnid orthogroup research
- Comparative genomics analysis
- Building mitochondrial genomes
- Genetics of adaptive phenotypes
- Spidroin genes and silk gland functions
- Sourcing phylogenetically informative markers
- Genetics of ecological niche diversification
- Evolution of climate resistance genes

2.3. Community survey has identified initial species for support

Figure 2 contains a summary of survey responses to the question “Which taxa could such a resource support that would benefit your research?”:

Figure 2: Desired taxa



Many respondents mentioned “spiders”, and *Parasteatoda tepidariorum* was specifically mentioned twice. Given the summary of available genomes in Table 1, the desire for chromosome-level genomes with a RefSeq annotation, and the extent of ongoing work pertaining to the species, *P. tepidariorum* (GCF_043381705.1) appears to be the best candidate species to initially include as it meets all of these criteria and was specifically requested.

Given that many researchers outlined a desire for both venom research and comparative genomics across arachnid orders, a scorpion species would make an excellent second addition. This is reflected in the responses from Figure 2. No currently available scorpion genome is chromosome-level, but *Centruroides vittatus* genome (GCF_030686945.1, scaffold-level) does have RefSeq annotation. This would make an excellent second species to include.

There also appears to be a desire for the inclusion of a jumping spider (Salticidae), and Opiliones are of interest. The survey has also revealed a desire for curated gene orthology between different arachnid orders, which could make the recently published uropygid (whip scorpion) genome an excellent candidate (*Mastigoproctus giganteus*, Kulkarni, Klementz, and Sharma 2025). These taxa will be considered during subsequent gradual rounds of onboarding for new taxa as resources allow.

2.4. Some computational infrastructure has been secured

Domain names for both arachnobase.org and arachnobase.com have been secured until 10th July 2031. LiteSpeed SOHO web hosting has been secured until 17th June 2028, and RapidSSL certification has been added for security. At the time of writing, the site can be visited and an “under construction” message can be seen, but data is not currently being hosted. The corresponding author has determined additional hardware needs from discussions with both Dell and Lenovo, along with representatives at other model organism resources (e.g. Xenbase, Fisher et al., 2023). The corresponding author has also been awarded HPC resources to pursue initial data analysis and curation ([Access Allocation Request BIO250127](#)).

3. ARACHNOBASE: SPECIFIC AIMS

3.1. Gene pages

Arachnobase aims to host data pertaining to specific genes across arachnids in the same way as other existing model organism databases, e.g. Echinobase, FlyBase, and Xenbase. The ability for users to search for specific genes of interest by their names, synonyms, and external IDs (e.g. Entrez) will be essential. These searches are intended to bring users to web pages containing all pertinent and available data for the gene they have searched for. This may include gene expression values from transcriptomes, gene ontology terms to assess function, genome browser visualizations of the architecture surrounding that gene, links to literature mentions of that gene, cross-linking with other databases, and more. These gene pages will be central to navigating the resource, and while they will not be the only data hosted on Arachnobase, the gene pages are intended to be the primary way that users interact with it.

3.2. Gene orthology mapping and gene identities

Generating gene pages will require knowledge of gene identities. Robust gene orthology mapping and gene annotation can resolve this, and is also a highly desired function for the resource (per Figure 1). While the arachnid situation is complicated by whole genome duplication events, Echinobase has found success in leveraging gene orthology between *Strongylocentrotus purpuratus* (the purple sea urchin) and humans to match echinoderm genes with a human equivalent (Foley et al., 2021), which later informs gene annotation and the curation of gene identities (Beatman et al., 2021). These processes are also compliant with standards defined by the Alliance of Genome Resources Consortium (2024). At Arachnobase, an extensive, pairwise gene orthology analysis between *P. tepidariorum* and each of human and *Drosophila* will be performed in a similar way, following a DIOPT-like process (Hu et al., 2011). This will form an initial set of gene identities from which gene pages may be constructed, depending on which analysis recovers more single copy ortholog matches. These genes will then inherit their corresponding human gene symbols and names at Arachnobase, and also be issued an Arachnobase-specific ID (hereafter ACB ID). For cases where an ortholog cannot be confidently assigned to a human match, as would likely be the case for spidroids

and some other gene families that are lineage-specific or rapidly evolving, the ACB ID will link orthologous genes within Arachnida and annotate them with gene ontology data.

When including further species, gene orthology investigations between *P. tepidariorum* and the proposed new inclusions will be conducted. From this, orthologous genes in other arachnids can inherit their *P. tepidariorum* gene symbols and share a gene page. This will place *P. tepidariorum* as a “central” species for Arachnobase, in the same way that FlyBase uses *D. melanogaster* as its central species.

Beyond gene page construction, access to accurate and curated gene orthology information is essential when assaying gene expression and function. This is important in supporting ongoing, emergent developmental studies, and in comparative genomics research. Arachnobase will also derive gene ontology information by using KEGG (Kanehisa et al., 2025), to describe and list putative gene functions on gene pages. This will assist biotechnology questions (e.g. [those listed in 2.1](#)) by offering knowledge of gene functions, additional gene targets, and whether orthologs exist in any non-arachnid systems (e.g. humans).

3.3. Genome browser tracks for visualization

To support studies in functional and regulatory genomics, Arachnobase proposes to host JBrowse on-site to visualize arachnid genomes. Beyond working towards hosting multiple-genome alignments for arachnids on Arachnobase, this framework also opens the possibility of hosting other high-quality datasets. In the case of *Parasteatoda tepidariorum*, many publicly available genome-wide datasets could be shared as genome-browser tracks on Arachnobase for greater utility and visibility (e.g. Iwasaki-Yokozawa et al., 2022; Akaiwa et al., 2025). Other datasets can also be hosted as they become available, e.g. RNA-Seq (for venom gland transcriptome datasets, etc.), ATAC-Seq, and eRNA data. Such data can be processed per Foley et al., 2021, which will also yield raw tracks that will be hosted for download on Arachnobase if the users would prefer an alternative to the on-site viewer.

3.4. FAIR principles and integrating with other resources

Arachnobase will ensure that data hosted on the resource will be compliant with FAIR principles (Findable, Accessible, Interoperable, and Reproducible). Adhering to this essential data standard will be achieved by enforcing consistent gene names and symbols, which will facilitate integration and cross-linking with external resources. Entrez IDs will be utilized on Arachnobase, which will allow them to be integrated with NCBI databases. In cases where literature is present on gene pages, links can be provided to the World Spider Catalog (2025) if they have that literature. There is also scope to leverage and deploy machine learning processes to automate part of the literature curation process (e.g. Karimi et al., 2021). Links to the SpiderTraitDB (Pekár, 2021) will also be included where appropriate, e.g. for cases where genes are confidently linked to a given phenotype. Adherence to FAIR principles will also facilitate accessible data for researchers globally, regardless of their funding status and resources. This is particularly important when one considers that arachnids are found in

abundance on all continents except Antarctica, and that Arachnabase will only require a web browser to use.

Arachnabase intends to be compliant with data standards outlined by the Alliance of Genome Resources Consortium (2024). This will expand the utility and value of arachnid datasets beyond just the arachnid research community. Arachnabase will also disseminate information that describes these standards to ensure that users are aware of the data quality requirements before requesting Arachnabase to pull and integrate that data.

3.5. Arachnid community hub

In addition to being the resource this research community will use to explore data to design and interpret experiments, model organism knowledgebases are also the hub where members go to obtain information on other members via a directory and events relevant to the community, such as conference announcements and breakthroughs in the literature. The system we propose to deploy following the successful experience of Echinobase has powerful dynamic features to display announcements and keep the user community informed and interconnected.

3.6. Additional Arachnabase functions

Support for on-site BLAST searching is intended for all integrated species at launch, along with assembly statistics for each genome. It is also hoped that Arachnabase can serve as a repository for some laboratory resources, e.g. data on experimental protocols, reagents, PCR primer data, and more depending on community requests. Laboratories generate large numbers of datasets in most modern publications, and these often disappear into data archives where they are impossible to locate, have no standardization with little if any metadata, and disappear and get lost over time as publisher web resources evolve. Providing long term data archiving, a requirement for many federal research grants, data management using FAIR principles, and linking these data to community members, publications and other data will leverage the value of these rich resources.

3.7. Future directions

In addition to gene and genome information, Arachnabase will work towards supporting community-driven datasets and initiatives, e.g. by hosting emergent single-cell / single-nucleus datasets (e.g. Akiyama-Oda et al., 2022; Jin et al., 2023; Leite et al., 2024; Medina-Jiménez et al., 2024; Akaiwa et al., 2025). This will be achieved by standardizing dataset submissions in accordance with the UCSC Cell Browser guidelines (Speir et al., 2021) to facilitate the visualization of single-cell data on-site and ensure that these datasets can be effectively utilized by users.

Functional regulatory datasets may also become available for arachnids in the coming years. For example, an ATAC-seq protocol has recently been established for *P. tepidariorum* (Erdoğan et al., 2025). Arachnabase will aim to develop support for such datasets and ensure that they will be interoperable with other databases. Support for JBrowse visualization and transcript quantification is also anticipated (e.g. per Foley et al., 2021).

Arachnabase is intended to be a community-driven resource. The corresponding author is eager to ensure that this remains the case, and is open to hearing any thoughts, feedback, and / or requests to ensure that the resource best serves the community. As such, Arachnabase will conduct yearly surveys once operational, and will aim to have a presence at international congresses to ensure that community needs are best-served, and that emerging needs are anticipated.

4. ADDITIONAL INFORMATION

4.1. ARACHNOBASE COMMUNITY MEMBERS (*LISTED ALPHABETICALLY*)

Alireza Zamani, University of Turku, Finland

Alistair McGregor, Durham University, United Kingdom

Chris Hamilton, University of Idaho, USA

Daniela C. Rößler, University of Bonn, Germany

Danniella Sherwood, University of Prishtina, Republic of Kosovo

Donard Geci, University of Prishtina, Republic of Kosovo

Fernando Pérez-Miles, Universidad de la República, Uruguay

Giulia Zancolli, University of Lausanne, Switzerland

Hiroki Oda, JT Biohistory Research Hall, Japan

Jeremy Wilson, Western Australian Museum, Australia

Kamran Karimi, University of Calgary, Canada

Lauren Sumner-Rooney, Leibniz Institute for Evolution and Biodiversity, Museum für Naturkunde, Germany

Mark Harvey, Western Australian Museum, Australia

Matthias Pechmann, University of Cologne, Germany

Michael Rix, Biodiversity and Geosciences Program, Queensland Museum, Australia

Natascha Turetzek, LMU Munich, Germany

Nico Posnien, University Goettingen, Germany

Peter Vize, University of Calgary, Canada

Prashant Sharma, University of Madison-Wisconsin, USA

Stano Pekár, Masaryk University, Czechia

Tim Lüddecke, Fraunhofer Institute for Molecular Biology and Applied Ecology, Germany

Vinodkumar Saranathan, IRBI, CNRS / University of Tours, France

Yasuko Akiyama-Oda, JT Biohistory Research Hall, Japan

Zachary Sylvain, Marian University, USA

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